

SEQUENCE LISTING

<110> Curtis, Rory A.J., Lora, Jose M.

<120> 46798, A HUMAN MATRIX METALLOPROTEINASE
AND USES THEREFOR

<130> MPI2001-014PlRCPl (M)

<150> 60/262,252

<151> 2001-01-16

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2310

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (317)...(1651)

<400> 1

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ccggctccg gcgaaggca gcggaggag gccccagagc gcgcagctag ggcactggcg 180
aaaccccgcc acagtccctc tccgtgcggg ggcggcgagc agcagctcca tccccgggg 240
cccgggcgcg gctgaactgc ggcgtgttcc ctgcgcgagc tagctcccc agccgggctg 300
caccggaggc ggcgag atg gtc gcg cgc gtc gcc ctc ctg ctg cgc gcc ctg 352
          Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu
          1              5              10

cag ctg cta ctg tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga 400
Gln Leu Leu Leu Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly
          15              20              25

ggc cag gag ctg cgc aag gag gcg gag gca ttc cta gag aag tac gga 448
Gly Gln Glu Leu Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly
          30              35              40

tac ctc aat gaa cag gtc ccc aaa gct ccc acc tcc act cga ttc agc 496
Tyr Leu Asn Glu Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser
          45              50              55              60

gat gcc atc aga gcg ttt cag tgg gtg tcc cag cta cct gtc agc gcc 544
Asp Ala Ile Arg Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly
          65              70              75

gtg ttg gac cgc gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg 592
Val Leu Asp Arg Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly
          80              85              90

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gtt aca gat acc aac agt tat gcg gcc tgg gct gag agg atc agt gac	640
Val Thr Asp Thr Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp	
95 100 105	
ttg ttt gct aga cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca	688
Leu Phe Ala Arg His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala	
110 115 120	
aag caa ggg ggc gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa	736
Lys Gln Gly Gly Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu	
125 130 135 140	
gcg cac ttc gac caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg	784
Ala His Phe Asp Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly	
145 150 155	
cgc aac ctg ttc gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc	832
Arg Asn Leu Phe Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly	
160 165 170	
ctc acc cac tcg ccc gcg ccg cgc gcg ctc atg gcg ccc tac tac aag	880
Leu Thr His Ser Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys	
175 180 185	
agg ctg ggc cgc gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg	928
Arg Leu Gly Arg Asp Ala Leu Leu Ser Trp Asp Val Leu Ala Val	
190 195 200	
cag agc ctg tat ggg aag ccc cta ggg ggc tca gtg gcc gtc cag etc	976
Gln Ser Leu Tyr Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu	
205 210 215 220	
cca gga aag ctg ttc act gac ttt gag acc tgg gac tcc tac agc ccc	1024
Pro Gly Lys Leu Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro	
225 230 235	
caa gga agg cgc cct gaa acg cag gcc cct aaa tac tgc cac tct tcc	1072
Gln Gly Arg Arg Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser	
240 245 250	
ttc gat gcc atc act gta gac agg caa cag caa ctg tac att ttt aaa	1120
Phe Asp Ala Ile Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys	
255 260 265	
ggg agc cat ttc tgg gag gtg gca gct gat ggc aac gtc tca gag ccc	1168
Gly Ser His Phe Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro	
270 275 280	
cgt cca ctg cag gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct	1216
Arg Pro Leu Gln Glu Arg Trp Val Gly Leu Pro Pro Pro Asn Ile Glu Ala	
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gcg gca gtg tca ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt	1264
Ala Ala Val Ser Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly	
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cga tgc tgg agg ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag 1312
 Arg Cys Trp Arg Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln
 320 325 330

ctg tgc cgg gca ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc 1360
 Leu Cys Arg Ala Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe
 335 340 345

ttc cct cct ctg cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac 1408
 Phe Pro Pro Leu Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr
 350 355 360

gtg ctg gcc cga ggg gga ctg caa gtg gag ccc tac tac ccc cga agt 1456
 Val Leu Ala Arg Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser
 365 370 375 380

ctg cag gac tgg gga ggc atc cct gag gag gtc agc gcc gcc ctg ccg 1504
 Leu Gln Asp Trp Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro
 385 390 395

agg ccc gat ggc tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc 1552
 Arg Pro Asp Gly Ser Ile Ile Phe Phe Arg Asp Arg Tyr Trp Arg
 400 405 410

ctc gac cag gcc aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc 1600
 Leu Asp Gln Ala Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr
 415 420 425

gag ctg ccc tgg atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg 1648
 Glu Leu Pro Trp Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu
 430 435 440

ttc tgaaggcacc tcctcacctc agaaactggt ggtgctctca gggcaaaatc 1701
 Phe
 445

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 tcaggacaca gagtggggagg gagactgatg caggcctacc agtccctggc tttttgtctg 2241
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 ggcggccgc 2310

<210> 2
 <211> 445
 <212> PRT
 <213> Homo sapiens

<400> 2
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Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu			
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu	20	25	30
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg	35	40	45
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg	50	55	60
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr	65	70	75
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg	85	90	95
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly	100	105	110
Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp	115	120	125
Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe	130	135	140
Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser	145	150	155
Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg	165	170	175
Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr	180	185	190
Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu	195	200	205
Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg	210	215	220
Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile	225	230	235
Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe	245	250	255
Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln	260	265	270
Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Val Ser	275	280	285
Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg	290	295	300
Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala	305	310	315
Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu	325	330	335
Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg	340	345	350
Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp	355	360	365
Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly	370	375	380
Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala	385	390	395
Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp	405	410	415
Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe	420	425	430
	435	440	445

<210> 3

<211> 1335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1335)

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tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg
20      25      30
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu

cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa
35      40      45
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu

cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga
50      55      60
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg

gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc
65      70      75      80
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg

gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc
85      90      95
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr

aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga
100      105      110
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg

cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggg ggc
115      120      125
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly

gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac
130      135      140
Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp

caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc
145      150      155      160
Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe

gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc ctc acc cac tcg
165      170      175
Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser

ccc gcg ccg cgc gcg ctc atg gcg ccc tac tac aag agg ctg ggc cgc
180      185      190

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Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
 gag cgc ctg ctc agc tgg gac gac gtg ctg gcc gtg cag agc ctg tat
 195 200 205
 Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr
 ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc cca gga aag ctg
 210 215 220
 Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
 ttc act gac ttt gag acc tgg gac tcc tac agc ccc caa gga agg cgc
 225 230 235 240
 Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
 cct gaa acg cag ggc cct aaa tac tgc cac tct tcc ttc gat gcc atc
 245 250 255
 Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
 act gta gac agg caa cag caa ctg tac att ttt aaa ggg agc cat ttc
 260 265 270
 Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
 tgg gag gtg gca gct gat ggc aac gtc tca gag ccc cgt cca ctg cag
 275 280 285
 Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln
 gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct gcg gca gtg tca
 290 295 300
 Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Val Ser
 ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg
 305 310 315 320
 Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Arg Cys Trp Arg
 ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag ctg tgc cgg gca
 325 330 335
 Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala
 ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc ttc cct cct ctg
 340 345 350
 Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu
 cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac gtg ctg gcc cga
 355 360 365
 Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg
 ggg gga ctg caa gtg gag ccc tac tac ccc cga agt ctg cag gac tgg
 370 375 380
 Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp
 gga ggc atc cct gag gag gtc agc ggc gcc ctg ccg agg ccc gat ggc
 385 390 395 400
 Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly
 tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc ctc gac cag gcc
 405 410 415

Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala
 aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg
 420 425 430
 Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp
 atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg ttc
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 Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe

<210> 4
 <211> 171
 <212> PRT
 <213> Artificial sequence

<400> 4
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 Gln Lys Phe Phe Gly Leu Pro Val Thr Gly Lys Leu Asp Ser Asn Thr
 35 40 45
 Leu Glu Val Met Lys Lys Pro Arg Cys Gly Val Pro Asp Val Gly Glu
 50 55 60
 Phe Arg Thr Phe Pro Gly Ser Pro Lys Trp Ser Lys Asn Asn Leu Leu
 65 70 75 80
 Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Arg Glu Asp Val
 85 90 95
 Asp Asp Ala Ile Arg Arg Ala Phe Gln Val Trp Ser Asp Val Thr Pro
 100 105 110
 Leu Thr Phe Thr Arg Val Ser Asp Gly Glu Ala Asp Ile Met Ile Ser
 115 120 125
 Phe Ala Arg Gly Glu His Gly Asp Phe Tyr Pro Phe Asp Gly Lys Gly
 130 135 140
 Gly Leu Leu Ala His Ala Phe Ala Pro Gly Pro Gly Ile Gly Ile Gly
 145 150 155 160
 Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
 165 170

<210> 5
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 5
 Ile Asp Ala Ala Phe Glu Asp Arg Asp Arg Gly Lys Thr Tyr Phe Phe
 1 5 10 15
 Lys Gly Asp Lys Tyr Trp Arg Phe Asp Pro Glu Thr Arg Gln Arg Val
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 Asp Pro Gly Tyr Pro Lys Leu Ile Ser Asp Leu Trp Pro Asp Gly Leu
 35 40 45
 Pro Cys
 50

<210> 6
 <211> 471

<212> PRT
<213> Homo sapiens

<400> 6

Met	His	Pro	Gly	Val	Leu	Ala	Ala	Phe	Leu	Phe	Leu	Ser	Trp	Thr	His
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Cys	Arg	Ala	Leu	Pro	Leu	Pro	Ser	Gly	Gly	Asp	Glu	Asp	Asp	Leu	Ser
			20					25						30	
Glu	Glu	Asp	Leu	Gln	Phe	Ala	Glu	Arg	Tyr	Leu	Arg	Ser	Tyr	Tyr	His
		35					40					45			
Pro	Thr	Asn	Leu	Ala	Gly	Ile	Leu	Lys	Glu	Asn	Ala	Ala	Ser	Ser	Met
		50				55					60				
Thr	Glu	Arg	Leu	Arg	Glu	Met	Gln	Ser	Phe	Phe	Gly	Leu	Glu	Val	Thr
				70							75			80	
Gly	Lys	Leu	Asp	Asp	Asn	Thr	Leu	Asp	Val	Met	Lys	Lys	Pro	Arg	Cys
				85					90					95	
Gly	Val	Pro	Asp	Val	Gly	Glu	Tyr	Asn	Val	Phe	Pro	Arg	Thr	Leu	Lys
			100					105					110		
Trp	Ser	Lys	Met	Asn	Leu	Thr	Tyr	Arg	Ile	Val	Asn	Tyr	Thr	Pro	Asp
		115					120					125			
Met	Thr	His	Ser	Glu	Val	Glu	Lys	Ala	Phe	Lys	Lys	Ala	Phe	Lys	Val
		130				135						140			
Trp	Ser	Asp	Val	Thr	Pro	Leu	Asn	Phe	Thr	Arg	Leu	His	Asp	Gly	Ile
		145				150					155			160	
Ala	Asp	Ile	Met	Ile	Ser	Phe	Gly	Ile	Lys	Glu	His	Gly	Asp	Phe	Tyr
				165					170					175	
Pro	Phe	Asp	Gly	Pro	Ser	Gly	Leu	Leu	Ala	His	Ala	Phe	Pro	Pro	Gly
			180					185					190		
Pro	Asn	Tyr	Gly	Gly	Asp	Ala	His	Phe	Asp	Asp	Asp	Glu	Thr	Trp	Thr
		195					200					205			
Ser	Ser	Ser	Lys	Gly	Tyr	Asn	Leu	Phe	Leu	Val	Ala	Ala	His	Glu	Phe
		210				215					220				
Gly	His	Ser	Leu	Gly	Leu	Asp	His	Ser	Lys	Asp	Pro	Gly	Ala	Leu	Met
					230					235				240	
Phe	Pro	Ile	Tyr	Thr	Tyr	Thr	Gly	Lys	Ser	His	Phe	Met	Leu	Pro	Asp
				245					250					255	
Asp	Asp	Val	Gln	Gly	Ile	Gln	Ser	Leu	Tyr	Gly	Pro	Gly	Asp	Glu	Asp
			260					265					270		
Pro	Asn	Pro	Lys	His	Pro	Lys	Thr	Pro	Asp	Lys	Cys	Asp	Pro	Ser	Leu
			275				280					285			
Ser	Leu	Asp	Ala	Ile	Thr	Ser	Leu	Arg	Gly	Gln	Thr	Met	Ile	Phe	Lys
			290				295				300				
Asp	Arg	Phe	Phe	Trp	Arg	Leu	His	Pro	Gln	Gln	Val	Asp	Ala	Glu	Leu
					310					315				320	
Phe	Leu	Thr	Lys	Ser	Phe	Trp	Pro	Glu	Leu	Pro	Asn	Arg	Ile	Asp	Ala
				325					330					335	
Ala	Tyr	Glu	His	Pro	Ser	His	Asp	Leu	Ile	Phe	Ile	Phe	Arg	Gly	Arg
			340					345					350		
Lys	Phe	Trp	Ala	Leu	Asn	Gly	Tyr	Asp	Ile	Leu	Glu	Gly	Tyr	Pro	Lys
			355				360					365			
Lys	Ile	Ser	Glu	Leu	Gly	Leu	Pro	Lys	Glu	Val	Lys	Lys	Ile	Ser	Ala
			370			375					380				
Ala	Val	His	Phe	Glu	Asp	Thr	Gly	Lys	Thr	Leu	Leu	Phe	Ser	Gly	Asn
				390						395				400	
Gln	Val	Trp	Arg	Tyr	Asp	Asp	Thr	Asn	His	Ile	Met	Asp	Lys	Asp	Tyr
				405					410					415	
Pro	Arg	Leu	Ile	Glu	Glu	Asp	Phe	Pro	Gly	Ile	Gly	Asp	Lys	Val	Asp


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          420          425          430
Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile
          435          440          445
Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
          450          455          460
Ala Asn Ser Ile Leu Trp Cys
          465          470

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```

<211> 10
<212> PRT
<213> Artificial Sequence

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<220>
<221> VARIANT
<222> (1)...(1)
<223> The amino acid at position 1 can be G, S, T, A, L,
      I, V, N.

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<223> Xaa at position 2 and 3 = any amino acid

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<221> VARIANT
<222> (6)...(6)
<223> The amino acid at position 6 can be L, I, V, M, F,
      Y, W.

```

```

<221> VARIANT
<222> (7)...(7)
<223> The amino acid at position 7 can not be D, E, H,
      R, K, P.

```

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<223> Xaa at position 9= any amino acid

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<221> VARIANT
<222> (10)...(10)
<223> The amino acid at position 10 can be L, I, V, M,
      F, Y, W, G, S, P, Q.

```

```

<400> 4
Xaa Xaa Xaa His Glu Xaa Xaa His Xaa Xaa
  1             5             10

```

```

<210> 8
<211> 2527
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (300)...(1862)

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<400> 8
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gcggaccgcg gggcaggcac tgcctgggct ggacgacgtc tggccggctc ccggcgaagg 120
gcagcgaggg agcgcgccag agcgcgcgag tagggcactg gcgaaccccc gggacagtcc 180

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ctctccgtgc	ggggg	cgcg	cagag	cagtc	ccatccccg	ggccccggc	gcggctgact	240
gccggctggt	tcctctgcgcg	cagtagctcc	ccgagccggg	ctgcaccgga	ggcgccgag			299
atg gtc gcg cgc gtc gcc ctc ctg ctg cgc gcc ctg cag ctg cta ctg								347
Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu Leu								
1 5 10 15								
tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg								395
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu								
20 25 30								
cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa								443
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu								
35 40 45								
cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga								491
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg								
50 55 60								
gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc								539
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg								
65 70 75 80								
gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc								587
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr								
85 90 95								
aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga								635
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg								
100 105 110								
cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggt aac								683
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Asn								
115 120 125								
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Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu								
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His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln								
145 150 155 160								
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Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr								
165 170 175								
ggc ccc gct gac atc cgg ctc acc ttc ttc caa ggg gac cac aac gat								875
Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp								
180 185 190								
ggg ctg ggc aat gcc ttt gat ggc cca ggg ggc gcc ctg gcg cac gcc								923
Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala								
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Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp								
210 215 220								

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Leu	Trp	Ser	Asn	Val	Ser	Ala	Leu	Glu	Phe	Trp	Glu	Ala	Pro	Ala	Thr
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Gly	Pro	Ala	Asp	Ile	Arg	Leu	Thr	Phe	Phe	Gln	Gly	Asp	His	Asn	Asp
			180					185					190		
Gly	Leu	Gly	Asn	Ala	Phe	Asp	Gly	Pro	Gly	Gly	Ala	Leu	Ala	His	Ala
		195				200					205				
Phe	Leu	Pro	Arg	Arg	Gly	Glu	Ala	His	Phe	Asp	Gln	Asp	Glu	Arg	Trp
	210					215					220				
Ser	Leu	Ser	Arg	Arg	Arg	Gly	Arg	Asn	Leu	Phe	Val	Val	Leu	Ala	His
	225				230					235				240	
Glu	Ile	Gly	His	Thr	Leu	Gly	Leu	Thr	His	Ser	Pro	Ala	Pro	Arg	Ala
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Leu	Met	Ala	Pro	Tyr	Tyr	Lys	Arg	Leu	Gly	Arg	Asp	Ala	Leu	Leu	Ser
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Trp	Asp	Asp	Val	Leu	Ala	Val	Gln	Ser	Leu	Tyr	Gly	Lys	Pro	Leu	Gly
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Gly	Ser	Val	Ala	Val	Gln	Leu	Pro	Gly	Lys	Leu	Phe	Thr	Asp	Phe	Glu
	290					295					300				
Thr	Trp	Asp	Ser	Tyr	Ser	Pro	Gln	Gly	Arg	Arg	Pro	Glu	Thr	Gln	Gly
	305				310					315				320	
Pro	Lys	Tyr	Cys	His	Ser	Ser	Phe	Asp	Ala	Ile	Thr	Val	Asp	Arg	Gln
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Gln	Gln	Leu	Tyr	Ile	Phe	Lys	Gly	Ser	His	Phe	Trp	Glu	Val	Ala	Ala
			340					345					350		
Asp	Gly	Asn	Val	Ser	Glu	Pro	Arg	Pro	Leu	Gln	Glu	Arg	Trp	Val	Gly
		355					360					365			
Leu	Pro	Pro	Asn	Ile	Glu	Ala	Ala	Val	Ser	Leu	Asn	Asp	Gly	Asp	
	370				375					380					
Phe	Tyr	Phe	Phe	Lys	Gly	Gly	Arg	Cys	Trp	Arg	Phe	Arg	Gly	Pro	Lys
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Pro	Val	Trp	Gly	Leu	Pro	Gln	Leu	Cys	Arg	Ala	Gly	Gly	Leu	Pro	Arg
				405					410					415	
His	Pro	Asp	Ala	Ala	Leu	Phe	Phe	Pro	Pro	Leu	Arg	Arg	Leu	Ile	Leu
			420					425					430		
Phe	Lys	Gly	Ala	Arg	Tyr	Tyr	Val	Leu	Ala	Arg	Gly	Gly	Leu	Gln	Val
		435					440					445			
Glu	Pro	Tyr	Tyr	Pro	Arg	Ser	Leu	Gln	Asp	Trp	Gly	Gly	Ile	Pro	Glu
	450					455					460				
Glu	Val	Ser	Gly	Ala	Leu	Pro	Arg	Pro	Asp	Gly	Ser	Ile	Ile	Phe	Phe
	465				470				475					480	
Arg	Asp	Asp	Arg	Tyr	Trp	Arg	Leu	Asp	Gln	Ala	Lys	Leu	Gln	Ala	Thr
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Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu	
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cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa	144
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu	
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cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga	192
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg	
50 55 60	
gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc	240
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg	
65 70 75 80	
gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc	288
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr	
85 90 95	
aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga	336
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg	
100 105 110	
cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggt aac	384
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Asn	
115 120 125	
aaa tgg tac aag cag cac ctc tcc tac cgc ctg gtg aac tgg cct gag	432
Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu	
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cat ctg ccg gag ccg gca gtt cgg ggc gcc gtg cgc gcc gcc ttc cag	480
His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln	
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Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr	
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Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp	
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Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala	
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Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp	
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ctc atg gcg ccc tac tac aag agg ctg ggc cgc gac gcg ctg ctc agc Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser 260 265 270	1115
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cct aaa tac tgc cac tct tcc ttc gat gcc atc act gta gac agg caa Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln 325 330 335	1307
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ctg ccc ccc aac att gag gct gcg gca gtg tca ttg aat gat gga gat Leu Pro Pro Asn Ile Glu Ala Ala Val Ser Leu Asn Asp Gly Asp 370 375 380	1451
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cca gtg tgg ggt ctc cca cag ctg tgc cgg gca ggg gcc ctg ccc cgc Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg 405 410 415	1547
cat cct gac gcc gcc ctc ttc ttc cct cct ctg cgc cgc ctc atc ctc His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu 420 425 430	1595
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gag atc ggt cac acg ctt ggc ctc acc cac tcg ccc gcg ccg cgc gcg Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala 245 250 255	768
ctc atg gcg ccc tac tac aag agg ctg ggc cgc gac gcg ctg ctc agc Leu Met Ala Pro Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser 260 265 270	816
tgg gac gac gtg ctg gcc gtg cag agc ctg tat ggg aag ccc cta ggg Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly 275 280 285	864
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Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His	
500 505 510	
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Ala Asn Ser Gly Ser Ala Leu Phe *	
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